SEQUENCE LISTING

<110> Reinherz, Ellis L.
Freund, Christian
Li, Jing
Nishizawa, Kazuhisa
Wagner, Gerhard

<120> Cloning and Characterization of a CD2
Binding Protein (CD2BP2)

<130> 1062.1021-004

<150> US 60/111,007
<151> 1998-12-04

<150> US 60/115,647
<151> 1999-01-13

<150> PCT/US99/26993
<151> 1999-11-15

<160> 25

<170> FastSEQ for Windows Version 4.0

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<212> DNA
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<222> (121)...(1143)

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atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
1 5 10 15

gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
20 25 30

ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
35 40 45

agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
50 55 60

atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
65 70 75 80

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agc gag ggg ggt ggt cgg atc aca ccc ttt aac ctg cag gag gag atg      408
Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
                 85                  90                  95

gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat      456
Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
            100                 105                 110

gct cag atc cga gac agc tgg ctg gac aac att gac tgg gtg aag atc      504
Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
        115                 120                 125

cgg gag cgg cca cct ggc cag cgc cag gcc tca gac tcg gag gag gag      552
Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
    130                 135                 140

gac agc ttg ggc cag acc tca atg agt gcc caa gcc ctc ttg gag gga      600
Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
145                 150                 155                 160

ctt ttg gag ctc cta ttg cct aga gag aca gtg gct ggg gca ctg agg      648
Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
                165                 170                 175

cgt ctg ggg gcc cga gga gga ggc aaa ggg aga aag ggg cct ggg caa      696
Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
            180                 185                 190

ccc agt tcc cct cag cgc ctg gac cgg ctc tcc ggg ttg gcc gac cag      744
Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
        195                 200                 205

atg gtg gcc cgg ggc aac ctt ggt gtg tac cag gaa aca agg gaa cgg      792
Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
    210                 215                 220

ttg gct atg cgt ctg aag ggt ttg ggg tgt cag acc cta gga ccc cac      840
Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
225                 230                 235                 240

aat ccc aca ccc cca ccc tcc ctg gac atg ttc gct gag gag ttg gcg      888
Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
                245                 250                 255

gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag      936
Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
            260                 265                 270

tcg cgg gga gat ggt ctg gtg gat gtg atg tgg gaa tat aag tgg gag      984
Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
        275                 280                 285

aac acg ggg gat gcc gag ctg tat ggg ccc ttc acc agc gcc cag atg     1032
Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
    290                 295                 300
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cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg 1080
Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
305 310 315 320

aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac 1128
Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
325 330 335

ttt gac ctc tac acc tgagcctgct gggggcccag tttggtgggc ccttctttcc 1183
Phe Asp Leu Tyr Thr
340

tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggccattttt 1243
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Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
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35 40 45
Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
50 55 60
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
65 70 75 80
Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
85 90 95
Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
100 105 110
Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
115 120 125
Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
130 135 140
Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
145 150 155 160
Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
165 170 175
Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
180 185 190
Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
195 200 205
Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
210 215 220
Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
225 230 235 240
Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
245 250 255
Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
260 265 270
Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
275 280 285
Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
290 295 300

Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
305 310 315 320
Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
325 330 335
Phe Asp Leu Tyr Thr
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<210> 3
<211> 26
<212> PRT
<213> Homo sapiens

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Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr
1 5 10 15
Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly
20 25

<210> 4
<211> 27
<212> PRT
<213> Caenorhabditis elegans

<400> 4
Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu
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Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly
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<210> 5
<211> 27
<212> PRT
<213> Caenorhabditis elegans

<400> 5
Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn
1 5 10 15
Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu
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<210> 6
<211> 27
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<213> Caenorhabditis elegans

<400> 6
Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu
1 5 10 15
Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn
20 25

<210> 7
<211> 29
<212> PRT

<213> Saccharomyces cerevisiae

<400> 7
Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
1 5 10 15
Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
20 25

<210> 8
<211> 27
<212> PRT
<213> Saccharomyces cerevisiae

<400> 8
Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
1 5 10 15
Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr
20 25

<210> 9
<211> 17
<212> PRT
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<223> Motif in CD2 binding region of CD2BP2

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<221> VARIANT
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<223> Xaa can be Tyr or Phe

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<223> Xaa can be Met or Val

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Phe

<210> 10
<211> 6

<212> PRT
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<220>
<223> CD2BP2 binding region

<400> 10
Pro Pro Pro Gly His Arg
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<210> 11
<211> 70
<212> PRT
<213> Homo sapiens

<400> 11
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1 5 10 15
Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
20 25 30
Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
35 40 45
Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
50 55 60
Leu Ser Pro Ser Ser Asn
65 70

<210> 12
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Kozak consensus sequence

<400> 12
ccgccacc 8

<210> 13
<211> 24
<212> DNA
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<220>
<223> Flag Epitope

<400> 13
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<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag Epitope

<400> 14
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 15
<211> 31
<212> PRT
<213> Gallus gallus

<220>
<223> Flag Epitope

<400> 15
Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Ser Asn
1 5 10 15
Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser
20 25 30

<210> 16
<211> 38
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Flag Epitope

<400> 16
Glu Val Thr Trp Glu Phe Lys Trp Ser Gln Asp Glu Thr Asp Ile Gln
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Gly Pro Phe Ser Thr Glu Lys Met Leu Lys Trp Ser Gln Glu Asn Thr
20 25 30
Arg Tyr Phe Lys Asn Gly
35

<210> 17
<211> 34
<212> PRT
<213> Leishmania major

<220>
<223> Flag Epitope

<400> 17
Val Trp Met Met Arg Trp Lys Ala Lys Pro Thr Val Gln His Gly Pro
1 5 10 15
Phe Thr Asp Asp Ala Ile Gln Gln Trp Gly Arg Asp Gly Tyr Phe Gly
20 25 30
Lys Lys

<210> 18
<211> 36
<212> PRT
<213> Caenorhabditis elegans

<220>
<223> Flag Epitope

<400> 18
Val Ile Asp Thr Lys Trp His Tyr Leu Gly Pro Asp Ser Glu Lys Tyr
1 5 10 15
Gly Pro Tyr Met Ser Lys Asp Met Leu Phe Trp Leu Gln Ala Gly Tyr
20 25 30
Phe Asn Asp Gly
35

<210> 19
<211> 35
<212> PRT
<213> Caenorhabditis elegans

<220>
<223> Flag Epitope

<400> 19
Val Glu Ser Ser Trp Arg Tyr Ile Asp Thr Gln Gly Gln Ile His Gly
1 5 10 15
Pro Phe Thr Ile Gln Met Met Ser Gln Trp Tyr Ile Gly Gly Tyr Phe
20 25 30
Ala Ser Thr
35

<210> 20
<211> 35
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223> Flag Epitope

<400> 20
Ile Glu Ser Gln Trp Lys Tyr Ile Asp Ser Asn Gly Asn Ile Gln Gly
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Pro Phe Gly Thr Asn Asn Met Ser Gln Trp Tyr Gln Gly Gly Tyr Phe
20 25 30
Thr Pro Thr
35

<210> 21
<211> 31
<212> PRT
<213> Saccharomces pombe

<220>
<223> Flag Epitope

<400> 21
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Val Asp Met His Gln Trp Tyr Arg Ala Gly Tyr Phe Pro Leu Gly
20 25 30

<210> 22
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 22
Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro
 1   5   10   15
Pro Pro Gly His Arg
            20

<210> 23
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 23
Asp Val Met Trp Glu Tyr Lys Trp Glu Asn Thr Gly Asp Ala Glu Leu
 1   5   10   15
Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly
            20   25   30
Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Pro Gly Gly
        35   40   45
Gln Phe Tyr Asn Ser Lys Arg Ile Asp Phe Asp Leu Tyr Thr
    50   55   60

<210> 24
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 24
Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Asn Asn
 1   5   10   15
Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser
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<210> 25
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 25

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 1               5                  10                  15
Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Ser Met Ser
            20                  25                  30
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